

#14



1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/900,237A

DATE: 05/07/2003
TIME: 13:58:19

TECH CENTER 1600/2900

MAY 15 2003

RECEIVED

Input Set : A:\BB-1170USCIP~1.txt
Output Set: N:\CRF4\05072003\I900237A.raw

3 <110> APPLICANT: Allen, Stephen M.
5 <120> TITLE OF INVENTION: Plant Cellulose Synthases
7 <130> FILE REFERENCE: BB1170 US CIP
9 <140> CURRENT APPLICATION NUMBER: US 09/900,237A
10 <141> CURRENT FILING DATE: 2001-07-06
12 <150> PRIOR APPLICATION NUMBER: US 60/092,844
13 <151> PRIOR FILING DATE: 1998-07-14
15 <150> PRIOR APPLICATION NUMBER: PCT/US99/15871
16 <151> PRIOR FILING DATE: 1999-07-13
18 <150> PRIOR APPLICATION NUMBER: 09/720383
19 <151> PRIOR FILING DATE: 2000-12-21
21 <160> NUMBER OF SEQ ID NOS: 33
23 <170> SOFTWARE: Microsoft Office 97
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1221
27 <212> TYPE: DNA
28 <213> ORGANISM: Hordeum vulgare
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32 catgccacca cgacctgtt tcaagggttc tgcgccaatc aatctctctg accgtctcaa 120
33 tcaagttctc cgggtgggtc ttgggtcagt tgaaattctg tttagcagac attgtcctat 180
34 ctggtacaat tacggtgggc ggttgaaact tctggagagg atggcttaca tcaacacccat 240
35 tgtttatcca ataacatccc ttccacttat cgcctattgt gtgcttctg ctatctgtct 300
36 cctcaccaac aaatttatca ttcccgagat cagtaactat gctgggatgt tctttattct 360
37 tatgtttgcc tccattttg ccacgggtat attggagctg cgatggagt gtgtcgcat 420
38 cgaggactgg tggagaaacg agcagttctg ggttattggt ggcacatctg cccatctttt 480
39 cgcagtgttc cagggtctgc tgaagggtgt ggccgggatt gacaccaact tcacggttac 540
40 ctcgaaggca aacgacgagg atggcgattt tgcgtagtta tacgtgttca agtggaccag 600
41 tctcctcatt cctccgacca cgcctcttgt gattaacctg gtgggcatgg tggcaggcat 660
42 atcatatgcc atcaacagcg gttaccagtc ttgggttcca ctcttcgaa agctcttctt 720
43 ctcaatctgg gtgatcctcc atctctaccc ctctctcaag ggtctcatgg ggaagcagaa 780
44 ccgcacgcca accatcgtca ttgtttggtc catctctcta gcctccatct tctccctcct 840
45 gtgggtgaag atcgacctt tcatatccga taccagaaa gccgtcgcca tggggcagtg 900
46 tggcgtaaac tgctgatcgg cgccgaagag tatctgcccc cctcgtgtaa ataccggagg 960
47 ggggttgatg ggattttgtt gttgtagatg aagacggagt tttatgtaag ttattattgc 1020
48 cccttcgtgc tgagaagcac aaaccgtgaa gcctacgaaa cctgcagcgt acattgtgat 1080
49 ttttttctcc ttttcttttc atctgtgata cctgtgtgtt cttcttagag tatattatgt 1140
50 cagaacgtat ctatagttct atacacacta tgacaccaac tatttatata aggcagctgt 1200
51 tgcatacaact cttctgcaaa a 1221
53 <210> SEQ ID NO: 2
54 <211> LENGTH: 304
55 <212> TYPE: PRT
56 <213> ORGANISM: Hordeum vulgare

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58 <400> SEQUENCE: 2

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63           20           25           30
65 Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly
66           35           40           45
68 Ser Val Glu Ile Leu Phe Ser Arg His Cys Pro Ile Trp Tyr Asn Tyr
69           50           55           60
71 Gly Gly Arg Leu Lys Leu Leu Glu Arg Met Ala Tyr Ile Asn Thr Ile
72   65           70           75           80
74 Val Tyr Pro Ile Thr Ser Leu Pro Leu Ile Ala Tyr Cys Val Leu Pro
75           85           90           95
77 Ala Ile Cys Leu Thr Asn Lys Phe Ile Ile Pro Glu Ile Ser Asn
78           100          105          110
80 Tyr Ala Gly Met Phe Phe Ile Leu Met Phe Ala Ser Ile Phe Ala Thr
81           115          120          125
83 Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu Asp Trp Trp
84           130          135          140
86 Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala His Leu Phe
87 145          150          155          160
89 Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn
90           165          170          175
92 Phe Thr Val Thr Ser Lys Ala Asn Asp Glu Asp Gly Asp Phe Ala Glu
93           180          185          190
95 Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro Thr Thr Val
96           195          200          205
98 Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser Tyr Ala Ile
99           210          215          220
101 Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe
102 225          230          235          240
104 Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly Leu Met
105           245          250          255
107 Gly Lys Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu
108           260          265          270
110 Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp Pro Phe Ile
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117 <211> LENGTH: 3776

118 <212> TYPE: DNA

119 <213> ORGANISM: Zea mays

121 <400> SEQUENCE: 3

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123 aagcgtgtcc ctcccctcc ctcaactccc ttctattcca tccccccca gacgcgcgcta 120
124 ccgcgcgcgc cgcacgcacg cttgccccgg gatctggaga tctggtagcg ccagggggat 180
125 ggaggccagc gccgggctgg tcgccggctc gcacaaccgg aacgagctcg tcgtcatccg 240
126 ccgcgatggc gagccagggc cgaagcccat ggaccagcgg aacggccagg tgtgccagat 300

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127 ttgcggcgac gacgtggggc gcaacccccga cggggagccg ttcgtggcct gcaacgagtg 360
128 cgccttcccc atctgccggg actgctacga gtacgagcgc cgcgagggca cgcagaactg 420
129 cccccagtgc aagaccgcct tcaagcgccct caaggggtgc gcgcgcgtgc ccggggacga 480
130 ggaggaggac ggcgtcgacg acctggagaa cgagttcaac tggagcgaca agcacgactc 540
131 ccagtacctc gccgagtcca tgctccacgc ccacatgagc tacggccgcg gcgccgacct 600
132 cgacggcgtg ccgcagccat tccacccccat ccccaatgtt cccctcctca ccaacggaca 660
133 gatggtcgat gacatccccg cgaccagca cgcccttggt cctcgttcg tgggtggcgg 720
134 ggggaagagg attcaccctc tcccgtagc ggatcccaac cttcctgtgc aaccgaggtc 780
135 tatggaccct tccaaggatc tcgccgcata tggctacggg agcgtagcat ggaaggagag 840
136 gatggagagc tggaagcaga agcaggagag gatgcaccag acgaggaacg atggcgggcg 900
137 cgatgatggt gatgatgcag atctaccact aatggatgaa gctagacagc cattgtccag 960
138 aaagatcccc cttccttcaa gccaaatcaa cccctatagg atgattataa taattcggct 1020
139 agtggttttg tgtttcttct tccactaccg agtgatgcac ccggtgcctg atgcatttgc 1080
140 tttatggctc atatctgtga tctgtgaaat ttggtttgcc atgtcttga tttctgacca 1140
141 gtttccaaag tggtttctta tcgagaggga aacctatctt gaccggctga gtttaagggt 1200
142 tgacaaggaa gggcatcctt ctcaactcgc ccctgttgat ttctttgtca gtacggttga 1260
143 tcccttgaag gaacctccat tggctactgc taatactgtt ctatctatcc tttcgggtga 1320
144 ttatccagtt gataaggttt catgctacgt ttctgatgat ggtgctgcca tgctgacatt 1380
145 tgaagcattg tctgaaacat ctgaatttgc aaagaaatgg gttcctttct gcaaaagata 1440
146 tagccttgag cctcgtgctc cagagtggta cttccaacag aagatagact acctgaaaga 1500
147 caaggtggcg ccaaactttg ttagagaacg gagagcaatg aagagagagt atgaggaatt 1560
148 caaggtcaga atcaatgcct tggttgctaa agcccaaaag gttcctgagg aaggatggac 1620
149 aatgcaggat ggaactccat ggcccggaaa taatgtccgt gatcatcctg gaatgattca 1680
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152 tgcattggct cgagtctctg ctgtactaac taatgctcct tatttgctga acttggattg 1860
153 tgatcactat atcaataata gtaaggctat aaaggaagca atgtgtttta tgatggatcc 1920
154 tttgcttgga aagaaagttt gctatgtgca gtttcctcaa agatttgatg ggattgatcg 1980
155 ccatgatcga tatgctaaca gaaatgttgt ctttttcgat atcaacatga aaggtttgga 2040
156 tggtatccag ggccaattt atgtgggtac tggatgtgtc ttcagaaggc aggcattata 2100
157 tggctacgat gctcccaaaa caaagaagcc accatcaaga acttgcaact gctggccaaa 2160
158 gtggtgcatt tgctgttgct gttttggtaa caggaagacc aagaagaaga ccaagacctc 2220
159 taaacctaaa tttgagaaga taaagaaact tttaagaaa aaggaaaatc aagcccctgc 2280
160 atatgctctt ggtgaaattg atgaagccgc tccaggagct gaaaatgaaa aggctagtat 2340
161 tgtaaatcaa cagaagtggg aaaagaaatt tggccagtct tcagtttttg ttgcatccac 2400
162 acttcttgag aatggtggaa ccctgaagag tgccagtcca gcttctcttc tgaagggaagc 2460
163 tatacatgtc atcagttgtg gatatgaaga caaaacaggc tggggaaaag atattggtt 2520
164 gatttatgga tcagtcacag aagatattct tactgggttt aagatgcact gccatggtt 2580
165 gcggtcaatt tactgcatac ctaaaacgggc cgccttcaaa ggttccgcac ctctcaatct 2640
166 ttccgatcgt cttcaccagg ttcttcgggt ggctcttggt tcaattgaaa ttttcttcag 2700
167 caaccactgc cctctctggt atgggtatgg tgggtgacta aagttcctgg aaaggttttc 2760
168 gtacattaac tccatcgat acccttggac atctatcccg ctcttggcct attgcacatt 2820
169 gcctgccatc tgcttgetga cagggaaatt tatcacgcca gagcttaaca atgttgccag 2880
170 cctctggttc atgtcacttt tcatctgcat ttttgctacg agcatcctgg aaatgagatg 2940
171 gagtgggtga ggcacgatg actggtggag aaacgagcag ttttgggtca ttggaggcgt 3000
172 gtcttcacat ctctttgctg tgttcagggt actcctcaag gtcatagctg gtgtagacac 3060
173 gagcttcact gtgacatcca agggcggaga cgacgaggag ttctcagagc tgtacacatt 3120
174 caaatggacg acccttctga tacctccgac aacctgctc ctactgaact tcattggagt 3180
175 ggtagctggc atctccaatg cgatcaacaa cgatattgaa tcatggggcc cctgttctcg 3240

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177 tgggaggcag aacaggacgc caacgattgt cattgtctgg tccatcctcc tggcttcgat 3360
178 cttctcgctg ctttgggtcc ggatcgaccc gttccttgcg aaggatgatg gtcccctgtt 3420
179 ggaggagtgt ggtctggatt gcaactagga ggtcagcacg tggacttccc cgtcagtgtg 3480
180 tggtcgaaga agtattttttg cagatgtttt gtgcccatat ttcttttttc aatttttgtc 3540
181 cctctgtaga tagaaacaag gggagaaggg gaaaaaaagt acttgtattt cttttgttcc 3600
182 atgggtggtg tgggtggtgg cggtcagcc tcgtgagtgc agtattgggc aaaccggagg 3660
183 ctgcggcaac cttgtgcagt tcggccacga atatactagg gaagatcgcg accaatcaat 3720
184 caatcgatga ccgagttcaa ttgttcagca aaaaaaaaaa aaaaaaaaaa aaaaaa 3776
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187 <211> LENGTH: 1148
188 <212> TYPE: PRT
189 <213> ORGANISM: Zea mays
191 <400> SEQUENCE: 4
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196 20 25 30
198 Pro Phe Pro Pro Arg Arg Arg Tyr Arg Arg Arg Arg Thr His Ala Cys
199 35 40 45
201 Pro Gly Ile Trp Arg Ser Gly Ser Ala Arg Gly Met Glu Ala Ser Ala
202 50 55 60
204 Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu Leu Val Val Ile Arg
205 65 70 75 80
207 Arg Asp Gly Glu Pro Gly Pro Lys Pro Met Asp Gln Arg Asn Gly Gln
208 85 90 95
210 Val Cys Gln Ile Cys Gly Asp Asp Val Gly Arg Asn Pro Asp Gly Glu
211 100 105 110
213 Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro Ile Cys Arg Asp Cys
214 115 120 125
216 Tyr Glu Tyr Glu Arg Arg Glu Gly Thr Gln Asn Cys Pro Gln Cys Lys
217 130 135 140
219 Thr Arg Phe Lys Arg Leu Lys Gly Cys Ala Arg Val Pro Gly Asp Glu
220 145 150 155 160
222 Glu Glu Asp Gly Val Asp Asp Leu Glu Asn Glu Phe Asn Trp Ser Asp
223 165 170 175
225 Lys His Asp Ser Gln Tyr Leu Ala Glu Ser Met Leu His Ala His Met
226 180 185 190
228 Ser Tyr Gly Arg Gly Ala Asp Leu Asp Gly Val Pro Gln Pro Phe His
229 195 200 205
231 Pro Ile Pro Asn Val Pro Leu Leu Thr Asn Gly Gln Met Val Asp Asp
232 210 215 220
234 Ile Pro Pro Asp Gln His Ala Leu Val Pro Ser Phe Val Gly Gly Gly
235 225 230 235 240
237 Gly Lys Arg Ile His Pro Leu Pro Tyr Ala Asp Pro Asn Leu Pro Val
238 245 250 255
240 Gln Pro Arg Ser Met Asp Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr
241 260 265 270
243 Gly Ser Val Ala Trp Lys Glu Arg Met Glu Ser Trp Lys Gln Lys Gln

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244          275          280          285
246 Glu Arg Met His Gln Thr Arg Asn Asp Gly Gly Gly Asp Asp Gly Asp
247          290          295          300
249 Asp Ala Asp Leu Pro Leu Met Asp Glu Ala Arg Gln Pro Leu Ser Arg
250 305          310          315          320
252 Lys Ile Pro Leu Pro Ser Ser Gln Ile Asn Pro Tyr Arg Met Ile Ile
253          325          330          335
255 Ile Ile Arg Leu Val Val Leu Cys Phe Phe Phe His Tyr Arg Val Met
256          340          345          350
258 His Pro Val Pro Asp Ala Phe Ala Leu Trp Leu Ile Ser Val Ile Cys
259          355          360          365
261 Glu Ile Trp Phe Ala Met Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp
262          370          375          380
264 Phe Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg Leu Ser Leu Arg Phe
265 385          390          395          400
267 Asp Lys Glu Gly His Pro Ser Gln Leu Ala Pro Val Asp Phe Phe Val
268          405          410          415
270 Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Val Thr Ala Asn Thr
271          420          425          430
273 Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys Val Ser Cys
274          435          440          445
276 Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu Ser
277          450          455          460
279 Glu Thr Ser Glu Phe Ala Lys Lys Trp Val Pro Phe Cys Lys Arg Tyr
280 465          470          475          480
282 Ser Leu Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gln Gln Lys Ile Asp
283          485          490          495
285 Tyr Leu Lys Asp Lys Val Ala Pro Asn Phe Val Arg Glu Arg Arg Ala
286          500          505          510
288 Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala Leu Val
289          515          520          525
291 Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Gln Asp Gly
292          530          535          540
294 Thr Pro Trp Pro Gly Asn Asn Val Arg Asp His Pro Gly Met Ile Gln
295 545          550          555          560
297 Val Phe Leu Gly Gln Ser Gly Gly His Asp Val Glu Gly Asn Glu Leu
298          565          570          575
300 Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Tyr Asn His
301          580          585          590
303 His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val
304          595          600          605
306 Leu Thr Asn Ala Pro Tyr Leu Leu Asn Leu Asp Cys Asp His Tyr Ile
307          610          615          620
309 Asn Asn Ser Lys Ala Ile Lys Glu Ala Met Cys Phe Met Met Asp Pro
310 625          630          635          640
312 Leu Leu Gly Lys Lys Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp
313          645          650          655
315 Gly Ile Asp Arg His Asp Arg Tyr Ala Asn Arg Asn Val Val Phe Phe
316          660          665          670

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/07/2003
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; Xaa Pos. 201

Seq#:19; N Pos. 262

Seq#:20; Xaa Pos. 88